

SEQUENCE LISTING

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<151> 2002-09-06

<150> GB 0304521.8

<151> 2003-02-27

<150> GB 0304657.0

<151> 2003-02-28

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<170> PatentIn version 3.1

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acg ccg aag ttc cgc gaa aaa ccg atg gaa aag gcg gtg ggc ctc acc	96
Thr Pro Lys Phe Arg Glu Lys Pro Met Glu Lys Ala Val Gly Leu Thr	
20 25 30	

tcc cgt ttt gat ttc gcc att cat gtg gcg cat gcc cgt tcc cgt ggt	144
Ser Arg Phe Asp Phe Ala Ile His Val Ala His Ala Arg Ser Arg Gly	
35 40 45	

ctg cgt cgg cgc atg cca ccg gtg ctg cgt cga cgg gct att gat gcg	192
Leu Arg Arg Arg Met Pro Pro Val Leu Arg Arg Arg Ala Ile Asp Ala	
50 55 60	

ctg ctg cag ggg ctg tgt ttc cac tat gac ccg ctg gcc aac cgc gtc	240
Leu Leu Gln Gly Leu Cys Phe His Tyr Asp Pro Leu Ala Asn Arg Val	
65 70 75 80	

cag tgt tcc atc acc aca ctg gcc att gag tgc gga ctg gcg aca gag	288
Gln Cys Ser Ile Thr Thr Leu Ala Ile Glu Cys Gly Leu Ala Thr Glu	
85 90 95	

tcc ggt gca gga aaa ctc tcc atc acc cgt gcc acc cgg gcc ctg acg	336
Ser Gly Ala Gly Lys Leu Ser Ile Thr Arg Ala Thr Arg Ala Leu Thr	
100 105 110	

ttc ctg tca gag ctg gga ctg att acc tac cag acg gaa tat gac ccg	384
Phe Leu Ser Glu Leu Gly Leu Ile Thr Tyr Gln Thr Glu Tyr Asp Pro	
115 120 125	

ctt atc ggg tgc tac att ccg acc gac atc acg ttc aca ctg gct ctg	432
Leu Ile Gly Cys Tyr Ile Pro Thr Asp Ile Thr Phe Thr Leu Ala Leu	
130 135 140	

ttt gct gcc ctt gat gtg tct gag gat gca gtg gca gct gcg cgc cgc	480
Phe Ala Ala Leu Asp Val Ser Glu Asp Ala Val Ala Ala Arg Arg	
145 150 155 160	

agt cgt gtt gaa tgg gaa aac aaa cag cgc aaa aag cag ggg ctg gat	528
Ser Arg Val Glu Trp Glu Asn Lys Gln Arg Lys Lys Gln Gly Leu Asp	
165 170 175	

acc ctg ggt atg gat gag ctg ata gcg aaa gcc tgg cgt ttt gtg cgt	576
Thr Leu Gly Met Asp Glu Leu Ile Ala Lys Ala Trp Arg Phe Val Arg	
180 185 190	

gag cgt ttc cgc agt tac cag aca gag ctt cag tcc cgt gga ata aaa 624
 Glu Arg Phe Arg Ser Tyr Gln Thr Glu Leu Gln Ser Arg Gly Ile Lys
 195 200 205

cgt gcc cgt gcg cgt cgt gat gcg aac aga gaa cgt cag gat atc gtc 672
 Arg Ala Arg Ala Arg Arg Asp Ala Asn Arg Glu Arg Gln Asp Ile Val
 210 215 220

acc cta gtg aaa cgg cag ctg acg cgt gaa atc tcg gaa gga cgc ttc 720
 Thr Leu Val Lys Arg Gln Leu Thr Arg Glu Ile Ser Glu Gly Arg Phe
 225 230 235 240

act gct aat ggt gag gcg gta aaa cgc gaa gtg gag cgt cgt gtg aag 768
 Thr Ala Asn Gly Glu Ala Val Lys Arg Glu Val Glu Arg Arg Val Lys
 245 250 255

gag cgc atg att ctg tca cgt aac cgc aat tac agc cgg ctg gcc aca 816
 Glu Arg Met Ile Leu Ser Arg Asn Arg Asn Tyr Ser Arg Leu Ala Thr
 260 265 270

gct tct ccc tga 828
 Ala Ser Pro.
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Ser Arg Phe Asp Phe Ala Ile His Val Ala His Ala Arg Ser Arg Gly
 35 40 45

Leu Arg Arg Arg Met Pro Pro Val Leu Arg Arg Arg Ala Ile Asp Ala
 50 55 60

Leu Leu Gln Gly Leu Cys Phe His Tyr Asp Pro Leu Ala Asn Arg Val
 65 70 75 80

8

Gln Cys Ser Ile Thr Thr Leu Ala Ile Glu Cys Gly Leu Ala Thr Glu
85 90 95

Ser Gly Ala Gly Lys Leu Ser Ile Thr Arg Ala Thr Arg Ala Leu Thr
100 105 110

Phe Leu Ser Glu Leu Gly Leu Ile Thr Tyr Gln Thr Glu Tyr Asp Pro
115 120 125

Leu Ile Gly Cys Tyr Ile Pro Thr Asp Ile Thr Phe Thr Leu Ala Leu
130 135 140

Phe Ala Ala Leu Asp Val Ser Glu Asp Ala Val Ala Ala Ala Arg Arg
145 150 155 160

Ser Arg Val Glu Trp Glu Asn Lys Gln Arg Lys Lys Gln Gly Leu Asp
165 170 175

Thr Leu Gly Met Asp Glu Leu Ile Ala Lys Ala Trp Arg Phe Val Arg
180 185 190

Glu Arg Phe Arg Ser Tyr Gln Thr Glu Leu Gln Ser Arg Gly Ile Lys
195 200 205

Arg Ala Arg Ala Arg Arg Asp Ala Asn Arg Glu Arg Gln Asp Ile Val
210 215 220

Thr Leu Val Lys Arg Gln Leu Thr Arg Glu Ile Ser Glu Gly Arg Phe
225 230 235 240

Thr Ala Asn Gly Glu Ala Val Lys Arg Glu Val Glu Arg Arg Val Lys
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Ala Ser Pro
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acagacagat atgca 195

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<400> 19
aattccccgt cgctgaggcg 20

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cgtaagccgg tactgattga 20

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